

SEQUENCE LISTING

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Clairmont, C.
Lin, S.
Belcourt, M.

<120> COMPOSITIONS AND METHODS FOR TUMOR-TARGETED
DELIVERY OF EFFECTOR MOLECULES

<130> 8002-059

<150> 60/157,581

<151> 1999-10-04

<150> 60/157,637

<151> 1999-10-04

<160> 61

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward primer

<400> 1

gaagatcttc cggaggaggg gaaatg

26

<210> 2

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer

<400> 2

cgggatccga gctcgagggc cgggaaagg atctaagaag atcc

44

<210> 3

<211> 477

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(474)

<400> 3

atg gta cgt agc tcc tct cgc act ccg tcc gat aag ccg gtt gct cat 48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
1 5 10 15

gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt 96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
20 25 30

cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctg cgt gat aac cag 144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
35 40 45

ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg 192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
50 55 60

ttc aag ggt cag ggc tgc ccg tgc act cat gtt ctg ctg act cac acc 240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
65 70 75 80

atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc 288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
85 90 95

gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg 336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
100 105 110

aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag 384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
115 120 125

aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat 432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
130 135 140

ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg 474
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

taa 477

<210> 4
<211> 158
<212> PRT
<213> Homo sapiens

<400> 4
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
1 5 10 15
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
20 25 30
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
35 40 45
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
50 55 60
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
65 70 75 80

Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
85 90 95
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
100 105 110
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
115 120 125
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
130 135 140
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

<210> 5
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 5 28
ccgacgcggtt gacacctgaa aactggag

<210> 6
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 6 29
ccgacgcgtg aaaggatctc aagaagatc

<210> 7
<211> 543
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(540)

<400> 7 48
atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc 96
Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
20 25 30

gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag 144
Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
35 40 45

ctg	cag	tgg	ctg	aac	cgt	cgc	gct	aac	gcc	ctg	ctg	gca	aac	ggc	gtt	192
Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	
50						55					60					

gag	ctc	cgt	gat	aac	cag	ctc	gtg	gta	cct	tct	gaa	ggg	ctg	tac	ctg	240
Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	
65					70					75					80	

atc	tat	tct	caa	gta	ctg	ttc	aag	ggg	cag	ggc	tgc	ccg	tcg	act	cat	288
Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	
			85					90						95		

gtt	ctg	ctg	act	cac	acc	atc	agc	cgt	att	gct	gta	tct	tac	cag	acc	336
Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	
			100					105					110			

aaa	gtt	aac	ctg	ctg	agc	gct	atc	aag	tct	ccg	tgc	cag	cgt	gaa	act	384
Lys	Val	Asn	Leu	Leu	Ser	Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	
	115						120					125				

ccc	gag	ggg	gca	gaa	gcg	aaa	cca	tgg	tat	gaa	ccg	atc	tac	ctg	ggg	432
Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	
	130					135					140					

ggc	gta	ttt	caa	ctg	gag	aaa	ggg	gac	cgt	ctg	tcc	gca	gaa	atc	aac	480
Gly	Val	Phe	Gln	Leu	Glu	Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	
145					150					155					160	

cgt	cct	gac	tat	cta	gat	ttc	gct	gaa	tct	ggc	cag	gtg	tac	ttc	ggg	528
Arg	Pro	Asp	Tyr	Leu	Asp	Phe	Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	
				165					170					175		

att	atc	gca	ctg	taa												543
Ile	Ile	Ala	Leu													
			180													

<210> 8

<211> 180

<212> PRT

<213> Artificial Sequence

<400> 8

Met	Lys	Lys	Thr	Ala	Ile	Ala	Ile	Ala	Val	Ala	Leu	Ala	Gly	Phe	Ala	
1				5					10					15		
Thr	Val	Ala	Gln	Ala	His	Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	
			20					25					30			
Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	
		35					40					45				
Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	
	50					55					60					
Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	
65				70					75					80		
Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	
			85					90						95		
Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	
			100					105					110			

Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
 115 120 125
 Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
 130 135 140
 Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
 145 150 155 160
 Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
 165 170 175
 Ile Ile Ala Leu
 180

<210> 9
 <211> 801
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<221> CDS
 <222> (1)...(798)

<400> 9
 atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct 48
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1 5 10 15
 acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac 96
 Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
 20 25 30
 aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt 144
 Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
 35 40 45
 tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa 192
 Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
 50 55 60
 gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc 240
 Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
 65 70 75 80
 tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct 288
 Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
 85 90 95
 ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act 336
 Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
 100 105 110
 ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat 384
 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
 115 120 125
 gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt 432
 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
 130 135 140

ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc 480
 Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
 145 150 155 160

atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga 528
 Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
 165 170 175

ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc 576
 Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
 180 185 190

caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg 624
 Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
 195 200 205

aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc 672
 Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
 210 215 220

tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga 720
 Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
 225 230 235 240

att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa 768
 Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
 245 250 255

gcc agt ttt ttc ggg gcc ttt tta gtt ggc taa 801
 Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
 260 265

<210> 10

<211> 266

<212> PRT

<213> Artificial Sequence

<400> 10

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1 5 10 15
 Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
 20 25 30
 Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
 35 40 45
 Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
 50 55 60
 Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
 65 70 75 80
 Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
 85 90 95
 Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
 100 105 110
 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
 115 120 125
 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
 130 135 140

Gly	His	Ser	Phe	Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val
145					150					155					160
Ile	His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg
				165					170						175
Phe	Gln	Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val
			180					185					190		
Gln	Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met
		195					200					205			
Lys	Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu
	210					215					220				
Tyr	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg
225				230						235					240
Ile	Phe	Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu
				245					250					255	
Ala	Ser	Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly						
			260					265							

<210> 11

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion construct

<221> CDS

<222> (1)...(462)

<400> 11

atg	aaa	aag	acg	gct	ctg	gcg	ctt	ctg	ctc	ttg	ctg	tta	gcg	ctg	act	48
Met	Lys	Lys	Thr	Ala	Leu	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Thr	
1				5					10					15		
agt	gta	gcg	cag	gcc	gct	cct	act	agc	tcg	agc	act	aag	aaa	act	caa	96
Ser	Val	Ala	Gln	Ala	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	
			20					25					30			
ctg	caa	ttg	gag	cat	ctg	ctg	ctg	gat	ctg	cag	atg	att	ctg	aat	ggc	144
Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	
			35				40						45			
atc	aat	aac	tac	aag	aac	cct	aag	ctg	act	cgc	atg	ctg	act	ttc	aaa	192
Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	
	50					55				60						
ttc	tac	atg	ccg	aaa	aag	gct	acc	gag	ctc	aaa	cat	ctc	cag	tgc	ctg	240
Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	
65					70					75					80	
gaa	gag	gaa	ctg	aag	ccg	ctg	gag	gaa	gta	ctt	aac	ctg	gca	cag	tct	288
Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	
				85					90					95		
aag	aac	ttc	cac	ctg	cgt	ccg	cgt	gac	ctg	atc	tcc	aac	atc	aat	gta	336
Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	
			100					105						110		

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac 384
 ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
 115 120 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc 432
 Ala Asp Glu Thr Ala Thr ile Val Glu Phe Leu Asn Arg Trp ile Thr
 130 135 140

ttt gcc caa tcg atc att agc acg tta act taa 465
 Phe Ala Gln Ser ile ile Ser Thr Leu Thr
 145 150

<210> 12
 <211> 154
 <212> PRT
 <213> Artificial Sequence

<400> 12
 Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr
 1 5 10 15
 Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
 20 25 30
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met ile Leu Asn Gly
 35 40 45
 ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
 50 55 60
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
 65 70 75 80
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
 85 90 95
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu ile Ser Asn ile Asn Val
 100 105 110
 ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
 115 120 125
 Ala Asp Glu Thr Ala Thr ile Val Glu Phe Leu Asn Arg Trp ile Thr
 130 135 140
 Phe Ala Gln Ser ile ile Ser Thr Leu Thr
 145 150

<210> 13
 <211> 465
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<221> CDS
 <222> (1)...(462).

<400> 13
 atg aaa cag tcg act ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act 48
 Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr
 1 5 10 15

Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
 115 120 125
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
 130 135 140
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
 145 150

<210> 15
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer

<400> 15
 agtctagaca atcaggcgaa gaacgg

26

<210> 16
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer

<400> 16
 agccatggag tcaccctcac ttttc

25

<210> 17
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer

<400> 17
 ggatccttaa gaccacttt cacatttaag t

31

<210> 18
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer

<400> 18
 gggtccatgg ttcacttttc tctatcac

28

<210> 19
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer

<400> 19
gtgtccatgg ggcacagcca ccgcgacttc cag 33

<210> 20
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 20
acacgagctc ctacttggag gcagtcatga agct 34

<210> 21
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 21
gtgtccatgg ctccggcgggc aagtgtcggg actgaccatc atcatcatca tcatcacagc 60
cacgcgact tc 72

<210> 22
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 22
gtgcggatcc ctacttggag gcagtcatga agctg 35

<210> 23
<211> 16
<212> PRT
<213> Homo sapiens

<400> 23
Met Ala Arg Arg Ala Ser Val Gly Thr Asp His His His His His His
1 5 10 15

<210> 24
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence TiP 13.40

<400> 24

Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg
 1 5 10 15
 Val Val Met Tyr Glu Gly
 20

<210> 25

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding TiP13.40

<400> 25

gcgtaccgct ggcgcctgtc ccatcgcccg aaaaccggct ttatccgcgt ggtgatgtac 60
 gaaggc 66

<210> 26

<211> 101

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 26

gtgtactagt gtggcgcagg cggcgtagcg ctggcgccctg tcccatcgcc cgaaaaccgg 60
 ctttatccgc gtgggtgatgt acgaaggcta aggatccgcg c 101

<210> 27

<211> 101

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 27

gcgcggatcc ttagccttcg tacatcacca cgcggataaa gccggttttc gggcgatggg 60
 acaggcgcca gcggtacgcc gctgcgcca cactagtaca c 101

<210> 28

<211> 101

<212> PRT

<213> Homo sapiens

<400> 28

Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro Gly Leu Leu Phe
 1 5 10 15
 Leu Gly Leu Leu Leu Leu Pro Leu Val Val Ala Phe Ala Ser Ala Glu
 20 25 30
 Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr Ser
 35 40 45
 Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly
 50 55 60
 Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg
 65 70 75 80

Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile Lys
 85 90 95
 Lys Leu Leu Glu Ser
 100

<210> 29
 <211> 106
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide

<400> 29
 cttcactagt gtggcgcagg cgaacggcgc caaatctgc ctggacctgc aggcgcgcgt 60
 gtacaaaaaa atcatcaaaa aactgctgga aagctaagga tccgcg 106

<210> 30
 <211> 106
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide

<400> 30
 cgcggtacct tagctttcca gcagtttttt gatgattttt ttgtacagcg gcgcctgcag 60
 gtccaggcag attttgcggc cgttcgcctg cgccacacta gtgaag 106

<210> 31
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 31
 Ile Tyr Ser Phe Asp Gly Arg Asp Ile Met Thr Asp Pro Ser Trp Pro
 1 5 10 15
 Gln Lys Val Ile Trp His Gly Ser Ser Pro His Gly Val Arg Leu Val
 20 25 30
 Asp Asn Tyr Cys Glu Ala Trp Arg Thr Ala Asp Thr Ala Val Thr Gly
 35 40 45
 Leu Ala Ser Pro Leu Ser Thr Gly Lys Ile Leu Asp Gln Lys Ala Tyr
 50 55 60
 Ser Cys Ala Asn Arg Leu Ile Val Leu Cys Ile Glu Asn Ser Phe Met
 65 70 75 80
 Thr Asp Ala Arg Lys
 85

<210> 32
 <211> 44
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide

<400> 32
 ggcttcacta gtgtggcgca ggcgatatac tcctttgatg gtcg 44

<210> 33
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 33
 cgcgggatcct tacttcctag cgtctgtcat gaaactg

37

<210> 34
 <211> 7117
 <212> DNA
 <213> E. coli

<400> 34

cccgggcact	tccggggcat	gagtatgtga	tatccggggc	tgcaccccg	accccgccaa	60
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<223> n=a, c, g, or t

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aac gcg ctg cag gaa gat acc ccg ccg ggc ccg tcc acc gtg ttt cgc 96
Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser Thr Val Phe Arg
15 20 25 30

ccg ccg acc tcc tcc cgc ccg ctg gaa acc ccg cat tgc cgc gaa atc 144
Pro Pro Thr Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile
35 40 45

cgc atc ggc atc gcg ggc atc acc atc acc ctg tcc ctg tgc ggc tgc 192
Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys
50 55 60

gcg aac gcg cgc gcg ccg acc ctg cgc tcc gcg acc gcg gat aac tcc 240
Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser
65 70 75

gaa aac acc ggc ttt aaa aac gtc ccg gat ctg cgc acc gat cag ccg 288
Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro
80 85 90

aaa ccg ccg tcc aaa aaa cgc tcc tgc gat ccg tcc gaa tat cgc gtc 336
Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val
95 100 105 110

tcc gaa ctg aaa gaa tcc ctg atc acc acc acc ccg tcc cgc ccg cgc 384
Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg
115 120 125

acc gcc cgc cgc tgc atc cgc ctc tgaaagcttg gctgttttgg cggatgagag 438
Thr Ala Arg Arg Cys Ile Arg Leu
130

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<210> 58

<211> 134

<212> PRT

<213> Bacteriophage

<400> 58

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Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile Arg Ile
35 40 45
Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys Ala Asn
50 55 60
Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser Glu Asn
65 70 75 80
Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro Lys Pro
85 90 95
Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val Ser Glu
100 105 110
Leu Lys Glu Ser Leu Ile Thr Thr Pro Ser Arg Pro Arg Thr Ala
115 120 125

Arg Arg Cys Ile Arg Leu
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<210> 59
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<223> n=a, c, g, or t

<221> CDS
<222> (7)...(427)

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Met-Ala-His-His-His-His-His-Tyr-Gly-Arg-Lys-Lys-Arg
1 5 10

cgt cag cgc cgt cgc atg aac gcg ctg cag gaa gat acc ccg ccg ggc 96
Arg Gln Arg Arg Arg Met Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly
15 20 25 30

ccg tcc acc gtg ttt cgc ccg ccg acc tcc tcc cgc ccg ctg gaa acc 144
Pro Ser Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr
35 40 45

ccg cat tgc cgc gaa atc cgc atc ggc atc gcg ggc atc acc atc acc 192
Pro His Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr
50 55 60

ctg tcc ctg tgc ggc tgc gcg aac gcg cgc gcg ccg acc ctg cgc tcc 240
Leu Ser Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser
65 70 75

gcg acc gcg gat aac tcc gaa aac acc ggc ttt aaa aac gtc ccg gat 288
Ala Thr Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp
80 85 90

ctg cgc acc gat cag ccg aaa ccg ccg tcc aaa aaa cgc tcc tgc gat 336
Leu Arg Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp
95 100 105 110

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